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DATE: 10/30/2002

PATENT APPLICATION: US/09/700,851A

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3 <110> APPLICANT: Matsumoto, Yoh-Ichi
 4 Kimura, Tsuyoshi
 5 Imaizumi, Atsuchi
 6 Takedo, Tae
 7 Co, May Sung
 8 Vasquez, Maximiliano
 9 TEIJIN LIMITED
 11 <120> TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE VEROTOXIN II AND
 12 CELL LINE PRODUCING SAME
 14 <130> FILE REFERENCE: 019026-000110US
 16 <140> CURRENT APPLICATION NUMBER: 09/700851A
 C--> 17 <141> CURRENT FILING DATE: 2002-07-23
 19 <150> PRIOR APPLICATION NUMBER: WO 99/59629
 20 <151> PRIOR FILING DATE: 1999-05-19
 22 <150> PRIOR APPLICATION NUMBER: US 60/086,570
 23 <151> PRIOR FILING DATE: 1998-05-20
 25 <160> NUMBER OF SEQ ID NOS: 8
 27 <170> SOFTWARE: PatentIn Ver. 2.1
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 31 <212> TYPE: DNA
 32 <213> ORGANISM: Mus musculus
 34 <220> FEATURE:
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 36 <222> LOCATION: (1)..(414)
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 39 <223> OTHER INFORMATION: Figure 1(A): Heavy chain variable region of mouse
 40 antibody VTm1.1 (MuVTm1.1).
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 45 1 5 10 15
 47 gtc cag tgt gaa gtg cag ctg gtg gag tcg ggg gga ggc tta gtg aag 96
 48 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
 49 20 25 30
 51 cct gga ggg ccc ctg aaa ctc tcc tgt gca gcc tct gga ttc act ttc 144
 52 Pro Gly Gly Pro Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 53 35 40 45
 55 agt agt tat ggc atg tct tgg gtt cgc cag act ccg gag aag agg ctg 192
 56 Ser Ser Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu
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 59 gag tgg gtc gca acc att agt act ggt ggt agt tac acc tac tac cca 240
 60 Glu Trp Val Ala Thr Ile Ser Thr Gly Gly Ser Tyr Thr Tyr Tyr Pro

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64 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
65          85          90          95
67 gcc ctg tat ctg caa atg agc agt ctg agg tct gag gac acg gcc ata 336
68 Ala Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Ile
69          100          105          110
71 tat tac tgt gca aga cgg ggg gac gca tgg ggt aac ttg gac tac tgg 384
72 Tyr Tyr Cys Ala Arg Arg Gly Asp Ala Trp Gly Asn Leu Asp Tyr Trp
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87 antibody VTm1.1 (MuVTm1.1).
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94 20 25 30
96 Pro Gly Gly Pro Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
97 35 40 45
99 Ser Ser Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu
100 50 55 60
102 Glu Trp Val Ala Thr Ile Ser Thr Gly Gly Ser Tyr Thr Tyr Tyr Pro
103 65 70 75 80
105 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
106 85 90 95
108 Ala Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Ile
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125 <221> NAME/KEY: CDS
126 <222> LOCATION: (1)..(381)
128 <220> FEATURE:
129 <223> OTHER INFORMATION: Figure 1(B): Light chain variable region of mouse
130 VTm1.1 antibody (MuVTm1.1).

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135 1 5 10 15
137 gcc tcc aga ggt gat gtt gtg cta act cag tct cca gcc acc ctg tct 96
138 Ala Ser Arg Gly Asp Val Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
139 20 25 30
141 gtg act cca gga gat agc gtc agt ctt tcc tgc agg gcc caa act 144
142 Val Thr Pro Gly Asp Ser Val Ser Leu Ser Cys Arg Ala Ser Gln Thr
143 35 40 45
145 att agc aac aac cta cac tgg tat caa cac aaa tca cat gag tct cca 192
146 Ile Ser Asn Asn Leu His Trp Tyr Gln His Lys Ser His Glu Ser Pro
147 50 55 60
149 agg ctt ctc atc aag tct gct tcc cag tcc atc tct ggg atc ccc tcc 240
150 Arg Leu Leu Ile Lys Ser Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser
151 65 70 75 80
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154 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn
155 85 90 95
157 agt gtg gaa act gaa gat ttt gga atg tat ttc tgt caa cag agt tac 336
158 Ser Val Glu Thr Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Tyr
159 100 105 110
161 agc tgg ccg ctc acg ttc ggt gct ggg acc aag ctg gag ctg aaa 381
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171 <220> FEATURE:

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173 VTml.1 antibody (MuVTml.1).

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182 Val Thr Pro Gly Asp Ser Val Ser Leu Ser Cys Arg Ala Ser Gln Thr
183 35 40 45
185 Ile Ser Asn Asn Leu His Trp Tyr Gln His Lys Ser His Glu Ser Pro
186 50 55 60
188 Arg Leu Leu Ile Lys Ser Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser
189 65 70 75 80
191 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn
192 85 90 95
194 Ser Val Glu Thr Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Tyr
195 100 105 110
197 Ser Trp Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
198 115 120 125

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212 <223> OTHER INFORMATION: Figure 2(A): Heavy chain variable region of
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218   1           5           10           15
220 gtc cag tgt gaa gtg caa ctg gtg gag tcg ggg gga ggc tta gtg cag      96
221 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
222           20           25           30
224 cct gga ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc act ttc     144
225 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
226           35           40           45
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229 Ser Ser Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
230           50           55           60
232 gag tgg gtc gca acc att agt act ggt ggt agt tac acc tac tac cca     240
233 Glu Trp Val Ala Thr Ile Ser Thr Gly Gly Ser Tyr Thr Tyr Tyr Pro
234           65           70           75           80
236 gac agt gtg aag ggt cga ttc acc atc tcc aga gac aat tcc aag aac     288
237 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
238           85           90           95
240 acc ctg tat ctg caa atg aac agt ctg agg gct gag gac acg gcc gta     336
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242           100          105          110
244 tat tac tgt gca aga cgg ggg gac gca tgg ggt aac ttg gac tac tgg     384
245 Tyr Tyr Cys Ala Arg Arg Gly Asp Ala Trp Gly Asn Leu Asp Tyr Trp
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270          35          40          45
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273          50          55          60
275 Glu Trp Val Ala Thr Ile Ser Thr Gly Gly Ser Tyr Thr Tyr Tyr Pro
276          65          70          75          80
278 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
279          85          90          95
281 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
282          100          105          110
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302 <223> OTHER INFORMATION: igure 2(B): Light chain variable region of
303 humanized VTml.1 antibody (HuVTml.1) .
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326 agg ttc agt ggc agt gga tca ggg aca gat ttc act ctc act atc agc 288
327 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
328 85 90 95
330 agt ctg gaa tct gaa gat ttt gca gtg tat tac tgt caa cag agt tac 336
331 Ser Leu Glu Ser Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Tyr
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335 Ser Trp Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

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VERIFICATION SUMMARY

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